

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 08:16:23 : Search time 4804 Seconds

(without alignments)
16756.528 Million cell updates/sec

US-10-054-680-1

Perfect score: 2766
Sequence: 1 atggcgcggttaagttgca.....gtcatcaaggggttctaa 2766

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Generating 1000000 45 summaries

Database: GenBank

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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2766.4	99.9	2966	6	AX480881 Sequence
2	2766.2	99.8	2966	6	AX480881 Sequence
3	2766.2	99.8	2966	6	AX480881 Sequence
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5	2657.6	98.1	2840	6	AX290471 Sequence
6	2352.4	85.0	4854	10	RNU5420
7	2290.2	82.8	3435	10	AF453257
8	1786.4	64.6	2534	9	HSNCX22
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ALIGNMENTS

RESULT 1	AX480881	Sequence	41 from Patent	2966 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	AX480881	Sequence	41 from Patent	2966 bp	DNA	linear	PAT 12-AUG-2002
DEFINITION	AX480881	Sequence	41 from Patent	2966 bp	DNA	linear	PAT 12-AUG-2002
ACCESSION	AX480881	Sequence	41 from Patent	2966 bp	DNA	linear	PAT 12-AUG-2002
VERSION	AX480881.1	GI:22217538					
KEYWORDS							
SOURCE							
ORGANISM							
human.							
Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.							
Lee, E.A., Baughn, M.R., Yue, H., Ding, L., Rauerman, B.E., Hafealla, A.J.,							
Khan, F.A., Nguyen, D.B., Elliott, V.S., Ramkumar, J., Walla, N.K.,							
Ison, C.H., Lu, Y., Gandhi, A.R., Warren, B.A., Duggan, B.M.,							

Tribouley, C. M., Burford, N., Lu, D. A., Lal, P. G., Yao, M. G., Xu, Y.,
Bruno, C. M., Thangavelu, K., Swarnakar, A., Tang, Y. T., Azimzai, Y.,
Thornton, M., Arvizu, C., and Policky, J. L.
Transporters and ion channels
Patent: WO 0246415-A 41 13-JUN-2002;
Incyte Genomics, Inc. (US)

FEATURES
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1. .2966
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 5923789CB1"

BASE COUNT 692 a 725 c 809 g 740 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Y 61 TTGTGCTCTTCCGTAATGGCTTCTGACAGAGGCTGGCTGAGGAGGAGCTCCAA 120
DB 261 TTGTGCTCTTCCGTAATGGCTTCTGACAGAGGCTGGCTGAGGAGGAGCTCCAA 320
OY 121 ACAGGCGAAGAATGAGTCTCTTCAAGGCTCATCGAGCTGCAAGAGGAGGCTCATCTG 180
DB 321 ACAGGCGAAGAATGAGTCTCTTCAAGGCTCATCGAGCTGCAAGAGGAGGCTCATCTG 380
OY 181 CCAATCTGTTACCCGGAACCTTCCCTTGGGACAAGATTGGCAGGGCTATTGTCTAT 240
DB 381 CCAATCTGTTACCCGGAACCTTCCCTTGGGACAAGATTGGCAGGGCTATTGTCTAT 440
OY 241 TTGTGCGCCGTAATGATGTTCTTGGGCTGCTCATCTGCTGACCGCTTATGCA 300
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OY 1681 ACAATCATGCTCCCTTTAGAGAGTGAAGGGAAGGCAAGGAGTGGGCTGAGAGCTT 1740
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LOCUS AX476818
DEFINITION Sequence 1 from Patent WO0233086.
ACCESSION AX476818
VERSION AX476818.1 GI:22216098
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1

AUTHORS Merkulov, G.V., Ketchum, K.A., Shao, W., Yan, C., di Francesco, V., and Beasley, E.M.
TITLE Isolated human transporter proteins, nucleic acid molecules encoding human transporter proteins, and uses thereof
JOURNAL Patent: WO 0233086-A 1 25-APR-2002;
PE Corporation (NY) (US)
FEATURES
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Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db	1930	GAGGAGGCCAAGAGATATAGCAGAGATGGGAABACCAGTATTTGGCTGAAACACCCAAAC	1988
Qy	1981	GAAGTCATCATTTGAGAGAGTCCCTATGATGATTCAGAAGTACAGGTGGACAACACTGATCAAGAG	2040
Db	1990	GAAGTCATCATTTGAGAGAGTCCCTATGATGATTCAGAAGTACAGGTGGACAACACTGATCAAGAG	2049
Qy	2041	ACAAACCTGGGCTGGTTGGTGGGGACCCATTTCTGAGAGGAGACAGTTCATTTGAGAGGCCATC	2100
Db	2050	ACAAACCTGGGCTGGTTGGTGGGGACCCATTTCTGAGAGGAGACAGTTCATTTGAGAGGCCATC	2109
Qy	2101	ACCGTCAGTCAGCAGAGGGGATGAGAGATGAGATGAATCCGGGGAGAGAGGCTGGCTCC	2160
Db	2110	ACCGTCAGTCAGCAGAGGGGATGAGAGATGAGATGAATCCGGGGAGAGAGGCTGGCTCC	2169
Qy	2161	TGCTTTGACTACGTCAATGACATTCCTGAGCTGTCTTCTGGAAGGTGCTGTTTGCTGTGTG	2220
Db	2170	TGCTTTGACTACGTCAATGACATTCCTGAGCTGTCTTCTGGAAGGTGCTGTTTGCTGTGTG	2229
Qy	2221	CCCCCACAAGATACGTGCACACAGGTGGGGCTGTGGGCGTGTCCATTCCTCATTCATTTGGC	2280
Db	2230	CCCCCACAAGATACGTGCACACAGGTGGGGCTGTGGGCGTGTCCATTCCTCATTCATTTGGC	2289
Qy	2281	ATGCTCACCGCCATCATTTGGGGGACCTGGCCCTGCACATTCGGGCTGCACATTTGGTCTCAA	2340
Db	2290	ATGCTCACCGCCATCATTTGGGGGACCTGGCCCTGCACATTCGGGCTGCACATTTGGTCTCAA	2349
Qy	2341	GATTCAGTCACAGCTGTTGTTTTCGTGGACATTTGGACACTCTGTGCCAGATACGTTTGCC	2400
Db	2350	GATTCAGTCACAGCTGTTGTTTTCGTGGACATTTGGACACTCTGTGCCAGATACGTTTGCC	2409
Qy	2401	AGCAAAGCTGTGGCCCTCCACAGAGATGTATAGCAGACAGCCCTCATTTGGCAAGGTGACAGGGC	2460
Db	2410	AGCAAAGCTGTGGCCCTCCACAGAGATGTATAGCAGACAGCCCTCATTTGGCAAGGTGACAGGGC	2469
Qy	2461	AGCAACGCGCTCAATATGCTTCTCTGGGACATGGGCTGGCTGGCTGGCCGACATTCAC	2520
Db	2470	AGCAACGCGCTCAATATGCTTCTCTGGGACATGGGCTGGCTGGCTGGCCGACATTCAC	2529
Qy	2521	TGGGCTCTGACAGGACACAGAGATTCCACAGTGTGGCCGACACACTGGCCTTCTCCGCTCAC	2580
Db	2530	TGGGCTCTGACAGGACACAGAGATTCCACAGTGTGGCCGACACACTGGCCTTCTCCGCTCAC	2589
Qy	2581	CTCTTCACACATCTTGGATTTGTCTGTGATCAGAGGTCCTCTTTGACCGAAGGGGCGCGAC	2640
Db	2590	CTCTTCACACATCTTGGATTTGTCTGTGATCAGAGGTCCTCTTTGACCGAAGGGGCGCGAC	2649
Qy	2641	CTGGAGAGGGAGAGCTTGGTGGGCCCCCGGTGGCTGCAACACTGGCCACAACATGCGCTTTGTG	2700
Db	2650	CTGGAGAGGGAGAGCTTGGTGGGCCCCCGGTGGCTGCAACACTGGCCACAACATGCGCTTTGTG	2709
Qy	2701	AGCGCTGGGCTCTCTACATATCTCTTGGCACACTAGAGGCGTATTTGCTACATCAAGGGG	2760
Db	2710	AGCGCTGGGCTCTCTACATATCTCTTGGCACACTAGAGGCGTATTTGCTACATCAAGGGG	2769
Qy	2761	TTTCTAA 2766	
Db	2770	TTTCTAA 2775	

RESULT 3	
HSA304853	2837 bp mRNA linear PRI 06-JUN-2001
LOCUS	
DEFINITION	Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative splice form B (SCL8A3 gene).
ACCESSION	AJ304853
VERSION	AJ304853.1 GI:14330384
KEYWORDS	alternative splicing; Form B; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1	(bases 1 to 2837)	Gabellini, N.	Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)	2	(bases 1 to 2837)	Bortoluzzi, S.	Direct Submission
3	(sodium/calcium exchanger)			8	member 3		Submitted (22-DEC-2000)
9				10			Department of Biological Chemistry, University of Padova, Via G. Colombo 3, 35131 Padova, ITALY
FEATURES	source	Location/Qualifiers					
gene	CDS	1..2837	/organism="Homo sapiens"				
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		/note="alternative splice form B (exons 2, 4, 5, 9, 10, 11, 12)"					
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		/db_xref="GI:14330385"					
		/translation="MAWLRLQPLTSAFLHGLVYFVLFLNGLRADSGSDVPSTGON					
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		EVITDSQREVITIKRPNGETSTTTIRVNEVTSNTLTMAISSAEIILSLIEVGHGF					
		IAGLGPSITVIGSAAFNMFIIGICVYVLPDGETRIKHLRFVETITAMSIFAVIMLY					
		MLIAVSPGVVQVEGLLTLEFFPVCLLAWADKRLFLFYKMKKRTDKHNGIILIE					
		TEGHPKGIEMDGKMNSHFLDGNLVLPEKGEVDESREMRILIKDKOKPEKDLDQ					
		LYEMANYALSHOOKSRAFYRIQATRMGTAGNLIKKHAADQAKKASMSVPHDEPD					
		DFISKVFPDPSYCLNCGAVLITVYRKGDMSKTYVDIKTEGDSAMPADFEFTE					
		GTVLAKGETQKESVGIIDDDIFEEDEHFFVRLSNRIEEOPEEKPMPAIFNSLP					
		PRVALASPCVATVITLDDDHAGIFTFPCDRIIHVSESIGVMEVKVLRISGAGTVIYP					
		RYVGTAKSGGGEDEDTYGELEFNDETVKIRYKIVDEEYERQENFIALGEPKMM					
		ERGISALLSPDRKLWEEBEARKLIAEMGKPVLEGHPRLKLEIIESEYEFKTVDKLTK					
		KTNIALVYLSHMRDQMEATVYAAAGDEDEBESGEPYVNHFLIPKVLFL					
		ACVPPEYCHGMACFAVSILIGKLIWIIIGDLASHECCTGLKDSYAVVAVFAGTGV					
		PDTFASKAAALQDVYADASIGNVTSNANVNFELIGLAWSVAAIYMAIQOEFVSAVG					
		TLAESVTLFTITFAFVFCISVLYRRRRPHLGGELGSRGCKLATIWLFLVSLMLTYILFATP					
		LEAFCYIKGF"					
BASE COUNT	668 a	697 c	779 g	693 t			
RIGIN							
Query Match	99.0%	Score 2737.4;	DB 9;	Length 2837;			
Best Local Similarity	99.5%;	Pred. No. 0;					
Matches 2760;	Conservative 0;	Mismatches 6;	Indels 9;	Gaps 1;			
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63	ATGGCGTGTTAAGTTTGCAGCGCTTCACACCTTCGCTTCCTTCATTTGGCGTGTAC	122					
61	TTTGTGCTTCCCTCAAAAGGCTTCTTGACACAGAGCGTGGTGGCTCGAGGAGCGTGC	120					
123	TTTGTGCTTCTTCTTAATGCTTCTTGACACAGAGCGTGGTGGCTCGAGGAGCGTGC	182					
121	ACAGGCGAGAACATAGTCTCTGTTCAGGCGTATCGGACTGCAAGAGAGGTGTCACTCG	180					
183	ACAGGCGAGAACATAGTCTCTGTTCAGGCGTATCGGACTGCAAGAGAGGTGTCACTCG	242					
181	CCAATCTGTACCCGAGAACCTTTCCTTGCGGACAAAGATTGGCAGGCTATTGTCTAT	240					
243	CCAATCTGTACCCGAGAACCTTTCCTTGCGGACAAAGATTGGCAGGCTATTGTCTAT	302					
241	TTTGTGCGCGTATTTACATGTCTCTTGCGGCGTCCATCATCTTGTGACCGCTCATGGCA	300					
303	TTTGTGCGCGCTGATTTACATGTCTCTTGCGGCGTCCATCATCTTGTGACCGCTCATGGCA	362					
301	TCTATTGAAGTCATCACCTCTTCAGAGAGGAGGTGACAAATTAAAGAAACCCATGAGAGA	360					

Db	363	TCCTATTTGAAAGTCATCACCTCTCTCAAGAGAGGAGGTACAAATTAGAAACCCCAATGTGA	422
Qy	361	ACAGACAAACCACTATTTCGGGTCGTGGAATGAAGATGTCTCCAAACCTGACCCCTTAATGGCC	420
Db	423	ACCAACACACCACTATTTCGGGTCGTGGAATGAAGATGTCTCCAAACCTGACCCCTTAATGGCC	482
Qy	421	CTGGGTTCTCTCTGCTCTGTGAGATACCTCTCTTTTAATTAAGAGTGTGTGTCATGGGTTTC	480
Db	483	CTGGGTTCTCTGCTCTGTGAGATACCTCTCTTTTAATTAAGAGTGTGTGTCATGGGTTTC	542
Qy	481	ATTGCTGTATCTTGGACCTCTTACCATTGTAGGAGTGCAGCCTTCACATGTTTCATC	540
Db	543	ATTGCTGTATCTTGGACCTCTTACCATTGTAGGAGTGCAGCCTTCACATGTTTCATC	602
Qy	541	ATCATTTGGACATCTGTGTCTGTACGTATCCAGACGGAGACATCGCAAGATCAAGCATCTA	600
Db	603	ATCATTTGGACATCTGTGTCTGTACGTATCCAGACGGAGACATCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTCTTCATCACCGCTGCTGGAGTATCTTGTCCCTACATCTGGCTCATATGAT	660
Db	663	CGAGTCTCTTCATCACCGCTGCTGGAGTATCTTGTCCCTACATCTGGCTCATATGAT	722
Qy	661	CTGGCAGTCTTCTCTCCCTGCTGTGTGTCTCAGGTTTGGGAAGCCCTCTCACTCTCTTC	720
Db	723	CTGGCAGTCTTCTCTCCCTGCTGTGTGTCTCAGGTTTGGGAAGCCCTCTCACTCTCTTC	782
Qy	721	TTTTCCAGTGTGTCTTCTTGGGCTGGGTGGCAGATTAACGACCTCTCTCTACAAATAC	780
Db	783	TTTTCCAGTGTGTGTCTTCTTGGGCTGGGTGGCAGATTAACGACCTCTCTCTACAAATAC	842
Qy	781	ATGCACAAAGATACCCGACAGACAAACCCAGAGATTTATATAGAGACAGAGGTTAC	840
Db	843	ATGCACAAAGATACCCGACAGACAAACCCAGAGATTTATATAGAGACAGAGGTTAC	902
Qy	841	CACCCCTAAGGGCATTTGATGATGATGGGAAATGATGAATTCCTCATTTCTAGATGGAAC	900
Db	903	CACCCCTAAGGGCATTTGATGATGATGGGAAATGATGAATTCCTCATTTCTAGATGGAAC	962
Qy	901	CTGGTGTCCCTGGGAAGGGAAGGAAGTGATGCCCGAGAGATGTGCCGAAATTC	960
Db	963	CTGGTGTCCCTGGGAAGGGAAGGAAGTGATGCCCGAGAGATGTGCCGAAATTC	1022
Qy	961	AAGGATCTGAAGCAAAAAACCCAGAGAGATTTAGATCACCTGGTGGAGATGGCCAA	1020
Db	1023	AAGGATCTGAAGCAAAAAACCCAGAGAGATTTAGATCACCTGGTGGAGATGGCCAA	1082
Qy	1021	TACTATGCTCTTTTCCACCAACAGAAAGCCGCGCTTCTACCGTATCCAAACCACTG	1080
Db	1083	TACTATGCTCTTTTCCACCAACAGAAAGCCGCGCTTCTACCGTATCCAAACCACTG	1142
Qy	1081	ATGATGACTGGTGCAGGCATATTCCTGTAGAAACATGCAAGCAACGCCAAAGAGCC	1140
Db	1143	ATGATGACTGGTGCAGGCATATTCCTGTAGAAACATGCAAGCAACGCCAAAGAGCC	1202
Qy	1141	TCCACATGACGAGGTGTCACACCGATGAGCCTGAGAGACTTTAATTTCCAAAGGTCCTTT	1200
Db	1203	TCCACATGACGAGGTGTCACACCGATGAGCCTGAGAGACTTTAATTTCCAAAGGTCCTTT	1262
Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACGTGTGGGGCTGTACTCTCTGACAAGTGTGAG	1260
Db	1263	GACCCATGTTCTTACCAAGTGCCTGGAGAACGTGTGGGGCTGTACTCTCTGACAAGTGTGAG	1322
Qy	1261	AAAGGGGAGACATGTCAAAAGACCATGTATGTGTGACTACAAAAACAGAGATGTCTGCC	1320
Db	1323	AAAGGGGAGACATGTCAAAAGACCATGTATGTGTGACTACAAAAACAGAGATGTCTGCC	1382
Qy	1321	AATGACAGGGGCTGACTATGAGTTTCACAGAGGAGCCGTTCTGTGAAGCCAGAGAGACC	1380
Db	1383	AATGACAGGGGCTGACTATGAGTTTCACAGAGGAGCCGTTCTGTGAAGCCAGAGAGACC	1442
Qy	1381	CAGAAAGGATTCCTCCGTGGGCATTAATTGATGACACATTTTGTAGAGAGATGAACATTC	1440

D	b	1443	CAGAAAGAGTTCCTCCGTTGGGCAATTAATTGATGACAGACATTTTGGAGGAGTGAACACTTC	1502
O	y	1441	TTTGTAGGTTGACCAATGTCCGATTAAGAGGACAGCCAGAGAGGGATGCTCTCA	1500
D	b	1503	TTTGTAGGTTGACCAATGTCCGATTAAGAGGAGACAGCCAGAGAGGGATGCTCTCA	1562
O	y	1501	GCAATATTCAACAGCTCTTCCCTTGCCGGGGCTGTGCTAGCCCTCCCTGTGTGGCCACA	1566
D	b	1563	GCAATATTCAACAGCTCTTCCCTTGCCGGGGCTGTGCTAGCCCTCCCTGTGTGGCCACA	1622
O	y	1561	GTTACACTCTTGATGTGATGACCAATGCAGGCACTTTCATTTTGAATGTATCTATTAT	1620
D	b	1623	GTTACACTCTTGATGTGATGACCAATGCAGGCACTTTCATTTTGAATGTATCTATTAT	1682
O	y	1621	GTCAGTGAGACTATTGTGTTATGTAGAGTTCAGAGTTCTCGGACATCAGTGCCCGGGGT	1680
D	b	1683	GTCAGTGAGACTATTGTGTTATGTAGAGTTCAGAGTTCTCGGACATCAGTGCCCGGGGT	1742
O	y	1681	ACAGTCATCCGTCCTTTTAGSACAGTAAAGGACACCCAAAGGTGTGGGTAGACATTT	1740
D	b	1743	ACAGTCATCCGTCCTTTTAGSACAGTAAAGGACACCCAAAGGTGTGGGTAGACATTT	1802
O	y	1741	GAAGACACATTTGGGGATTTGGAATTCAGAAATGAAGAACTGTAAACCAATAGGGTT	1800
D	b	1803	GAGACACATTTGGGGATTTGGAATTCAGAAATGAAGAACTGTAAACCAATAGGGTT	1862
O	y	1801	AAATATAGTATGATGAGGAGAAATCGAAAGGCAAGAAATTTTCTATTTCCCTTGCTGA	1860
D	b	1863	AAATATAGTATGATGAGGAGAAATCGAAAGGCAAGAAATTTTCTATTTCCCTTGCTGA	1922
O	y	1861	CCGAATGTGATGAACTGGCAATTCAGATGT-----GACGACAGAGACTGACT	1911
D	b	1923	CCGAATGTGATGAACTGGCAATTCAGATGT-----GACGACAGAGACTGACT	1982
O	y	1912	ATGGAAGAAGAGGAGCCCAAGAGAGATATGAGAGATGGGAAGCCAGTATTTGGGTAAAC	1971
D	b	1983	ATGGAAGAAGAGGAGCCCAAGAGAGATATGAGAGATGGGAAGCCAGTATTTGGGTAAAC	2042
O	y	1972	CCCAACTAGAAGTTCATATTGAAGAGTCTTATAGTTCAAGACTACGGTGGACAACTG	2031
D	b	2043	CCCAACTAGAAGTTCATATTGAAGAGTCTTATAGTTCAAGACTACGGTGGACAACTG	2102
O	y	2032	ATCAAGAAGACAAACCTGGCTTGTGTGTGGGACCCATTTCTGGAAGGACCAATTCATG	2091
D	b	2103	ATCAAGAAGACAAACCTGGCTTGTGTGTGGGACCCATTTCTGGAAGGACCAATTCATG	2162
O	y	2092	GAGGCCATCACCCGTACGTGACAGCAGGAGGATGAGATATGAATATCCGGGACGAGAGG	2151
D	b	2153	GAGGCCATCACCCGTACGTGACAGCAGGAGGATGAGATATGAATATCCGGGACGAGAGG	2222
O	y	2152	CTGCCCTCTCTTGTGACTACGTATGCACTTCTGACGTCTTCTGGAAGGTGCTGTTT	2211
D	b	2223	CTGCCCTCTCTTGTGACTACGTATGCACTTCTGACGTCTTCTGGAAGGTGCTGTTT	2282
O	y	2212	GCCGTGTGGCCCCCACAAGATACGTCCAGCGCTGGGCTGCTTGGCGGTCTCCATCTCTC	2271
D	b	2283	GCCGTGTGGCCCCCACAAGATACGTCCAGCGCTGGGCTGCTTGGCGGTCTCCATCTCTC	2342
O	y	2272	ATCATTTGGCATGCTCACCGCATCATTTGGGGACCTGGGCTGCCACATGGGCTGCACCAT	2331
D	b	2343	ATCATTTGGCATGCTCACCGCATCATTTGGGGACCTGGGCTGCCACATGGGCTGCACCAT	2402
O	y	2332	GGGTCTCAAAAGATTACGTACACAGCTGTGTGTTTCTGTGGCAATTTTGGCACTGTCCCAAT	2391
D	b	2403	GGGTCTCAAAAGATTACGTACACAGCTGTGTGTTTCTGTGGCAATTTTGGCACTGTCCCAAT	2462
O	y	2452	GTTGACGGGACAGCAAGCGCGTCAATGTCTTCTGTGGGACATGGGCTGTGGCTGTGGCC	2511
D	b	2573	GTTGACGGGACAGCAAGCGCGTCAATGTCTTCTGTGGGACATGGGCTGTGGCTGTGGCC	2582

[illegible]

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Oy 121 ACAGGGCAGAACATGAGTCTGTTCAGGGTATCGAGCTGCAAGAGGGTGCATTCG 180
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Oy 181 CCAATCTGTATCCCGAGAACCCCTTCCCTTGGGGACAGATTTCCAGGGTCAATGTCTAT 240
Db 181 CCAATCTGTATCCCGAGAACCCCTTCCCTTGGGGACAGATTTCCAGGGTCAATGTCTAT 240
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Oy 421 CTGGGTTCTCTGCTCTGAGATACTCTCTTTTAATGAGGTGTGTATGGGTTC 480
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Oy 481 ATTGCTGTGATCTGGGACCTTCTACATTTGAGGAGTGCAGCTTCAACATGTTTCATC 540
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Oy 1321 AATGACGGGCTGACTATGATGATTCACAGAGGGCAGCGTGTCTGAGAGCAGAGAGAC 1380
Db 1321 AATGACGGGCTGACTATGATGATTCACAGAGGGCAGCGTGTCTGAGAGCAGAGAGAC 1380
Oy 1381 CAGAGAGAGTCTCCGTGGGCTAATTTGATGACGACATTTTGAAGAGGATGACACTTC 1440
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Db 1741 GAGAGACATATGAGGAGTGTGAATTAAGAAATGATGAATCTGTGAATTAAGAGTT 1800
Oy 1801 AAAATGATGATGAGGAGATACGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
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Oy 1861 CCGAAATGATGAG 1902
Db 1861 CCGAAATGATGAG 1902
Oy 1903 AAGCTGACTATGAG 1962
Db 1903 AAGCTGACTATGAG 1962
Oy 1921 AAGCTGACTATGAG 1980
Db 1921 AAGCTGACTATGAG 1980
Oy 1963 GGTGAACACCCCAACTAGAGTCAATGGAAGTCTTATGACTTCAAGACTACGTTG 2022
Db 1963 GGTGAACACCCCAACTAGAGTCAATGGAAGTCTTATGACTTCAAGACTACGTTG 2022
Oy 2023 GACAAATGATCAAG 2082
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Oy 2041 GACAAATGATCAAG 2100
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Oy 2101 CAGTTTCATGAG 2160
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Oy 2143 GAGAGAGGCTGCTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2202
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Oy 2161 GAGAGAGGCTGCTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Db 2161 GAGAGAGGCTGCTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2220

QY 2203 GTGCTGTTTGGCTGTGTGTCCTGACAGAGTACTGCCACGGCTGGCCCTTTCGCCGTC 2262
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Db 2221 GTGCTGTTTGGCTGTGTGTCCTGACAGAGTACTGCCACGGCTGGCCCTTTCGCCGTC 2280
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QY 2263 TCCATCTCTATCTATGTCATGTCACCGCCATCATTTGGGACCTGGCCTTGCACCTTGGC 2222
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Db 2761 TATTGCTACATCAAGGGGCTTC 2781
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RESULT 5
HSA304852 2840 bp mRNA linear PRI 06-JUN-2001
LOCUS HSA304852
DEFINITION Homo sapiens mRNA for sodium/calcium exchanger SCL8A3, alternative
splice form A (SCL8A3 gene).
ACCESSION AJ304852.1 GI:14330382
VERSION 1
KEYWORDS Sodium/calcium exchanger.
human.
URCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2840)
AUTHORS Gabelini, N.
TITLE Characterization of the human SCL8A3 gene for solute carrier family
8, member 3 (sodium/calcium exchanger)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2840)
AUTHORS Bortoluzzi, S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and
Department of Biological Chemistry, University of Padova, via G.
Colombo 3, 35131 PADOVA, ITALY

FEATURES
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Location/Qualifiers

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CDS

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11, 12)"

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BASE COUNT 668 a 700 c 775 g 697 t
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Query Match 96.1%; Score 2657.6; DB 9; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;

Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

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Dp	783	TTTCCAGATGTGTCTCTCTTGGCTGGGTGGCAGATTAACGACTGCTCTTCTACAAATAC	842
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Dp	843	ATGCACAAAAAGTACCGCACACAAACCCGAGGATTTATCATATGAGACAGAGGTGAC	902
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Db	2343	CTCATCATTTGGCATGCTCACCGGCATCATTTGGGGACCTGCGCCATCTGGCGTGACAC	2402
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Db	2703	AGGGGGCGGCACCTGGGAGGGGAGCTTGGTGGGCGCCCGTGGCTGCAACTGTGCCACAACA	2762
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RNUM3420 4854 bp mRNA linear ROD 04-OCT-1996
LOCUS Rattus norvegicus sodium-calcium exchanger form 3 (NCX3) mRNA,
DEFINITION complete cds.
ACCESSION U53420
VERSION U53420.1 GI:1552525
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4854)
AUTHORS Nicoll,D.A., Quedanu,B.D., Qui,Z., Xia,Y.R., Lusis,A.J. and
Phillipson,K.D.
TITLE Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3
J. Biol. Chem. 271 (40), 24914-24921 (1996)
MEDLINE 96394663
PUBMED 8798769
REFERENCE 2 (bases 1 to 4854)
AUTHORS Nicoll,D.A. and Phillipson,K.D.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1996) Physiology, University of California, Los
Angeles, 3645 MRLB, 675 Circle Dr. S., Los Angeles, CA 90095-1760,
USA

FEATURES
Source

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BASE COUNT 1162 a 1216 c 1267 g 1209 t
ORIGIN

Query Match 85.0% Score 2352.4; DB 10; Length 4854;
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Matches 2525; Conservative 0; Mismatches 241; Indels 18; Gaps 1;
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LOCUS
DEFINITION Mus musculus sodium/calcium exchanger (Slc8a3) mRNA, complete cds.
ACCESSION AF453257
VERSION AF453257.1 GI:17432810
KEYWORDS
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Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
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TITLE Towards complete inventory of calcium transporters of the house
mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3435)
AUTHORS Kraev, A.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2001) Mt. Sinai Hospital, Samuel Lunenfeld
Research Institute, 600 University Avenue, Toronto, Ontario M5G
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BASE COUNT 745 a 900 c 988 g 802 t

ORIGIN

Query Match 82.8%; Score 2290.2; DB 10; Length 3435;
Best Local Similarity 89.3%; Pred. No. 0;
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DEFINITION	Sequence 3 from Patent WO0233086.				
ACCESSION	AX476820				
VERSION	AX476820.1	GI:22216099			
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ORGANISM	Homo sapiens				
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AUTHORS	1 Merkulov, G.V., Ketchum, K.A., Shao, W., Yan, C., di Francesco, V. and Beasley, E.M.				
TITLE	Isolated human transporter proteins, nucleic acid molecules encoding human transporter proteins, and uses thereof				
JOURNAL	Patent: WO 0233086-A 3 25-APR-2002;				
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DEFINITION Homo sapiens Na+/Ca2+ exchanger isoform 3 (SLC8A3) gene, promoter
region and complete cds.
ACCESSION AF508982
VERSION AF508982.1 GI:22087482
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
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REFERENCE
1 (bases 1 to 145118)
Gabelini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.
CONTROL OF THE Na+/Ca2+ EXCHANGER 3 PROMOTER BY cAMP AND Ca2+ IN
DIFFERENTIATING NEURONS
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 145118)
Gabelini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.
TITLE The human Na+/Ca2+ exchanger 3 gene (SLC8A3) and spliced isoforms
AUTHORS 3 (bases 1 to 145118)
Gabelini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.
TITLE Direct Submision
JOURNAL Submitted (02-MAY-2002) Department of Biology, University of
Padova, via G. Colombo 3, Padova, PD 35131, Italy
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone Rp11-1111
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 146055)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
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Wheeler,O., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
Direct Submission
Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7321520.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1464
Center clone name: L111
----- Summary Statistics
Sequencing vector: M13, M77815, 99% of reads
Sequencing method: Plasmid; n/a; 8-0.1% of reads
Chemistry: Dye-terminator Big Dye; 94% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 126247 bases at least Q40
Consensus quality: 138332 bases at least Q20
Insert size: 160000; agarose-gel
Insert size: 143055; sum-of-coverage
Quality coverage.
* NOTE: This is a 'working draft' sequence. It currently

FEATURES
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* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Db	113956	AATGACAGGCGAGCACTATGATTTCTACAGAGAGGCACTGTGGTTCTGAAGCCAGAGAGAGACC	114015
QY	1381	CAGAAAGGAGTCTCCCGTGGGCATATATGATGACGACATTTTGAAGAGATGAACACTTC	1440

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Db 1603 GACACGCGGCGCATTTTCTTTGAGGAACCTGTGACATCATGTGATGAGACANTGGC 1662
Qy 1639 GTTATGAGAGTCAAGGTTTGGCGACATCAGTCCCGGGGTACACTCATCTGCCCTTT 1698
Db 1663 ATCATGAGAGTAAAGATATGTAGAACATCTGGAGCTCGGAAATGTATCTCCCTCAT 1722
Qy 1699 AGCAGATGAGAGGACACCAAGGGTGGCGGTGAGGACATTGAGACATATGGGGAG 1758
Db 1723 AAAACCATCGAAGGAGCTGCCAGAGGTGGAGGGAGATTGAGACACTGTGGAGAG 1782
Qy 1759 TTGAATTCAGAAATGATGAAACTGTGAAACCATAGGGTTAAATAGTAGATGAGAG 1818
Db 1783 CTGCAATTCAGAAATGATGAAATTTGAGAGATCATTTACATTAGAATATTGACGTGAG 1842
Qy 1819 GAATACGAAAGGCAAGAGATTTCTTCATTCCTTGGTGAACCGAATGATGAGACGT 1878
Db 1843 GAATATGAGAAAGATGTGAGTTCTCCCTGTCTGAGGAACCAAAATGATAGAGAGA 1902
Qy 1879 GGAATATCAG-----ATGTACAGACAGAGAGCTGACTATG 1914
Db 1903 GGAATGAAAGTGGCTTCAATTAACAGACGAATATGATGACAGCAGCCACTGACACG 1962
Qy 1915 GAAGAAGAGAGGCCAAGAGATAGCAGATGGGAAAGCCAGTATGGGTGAACACCC 1974
Db 1963 AAAGAGGAAAGAGAGAGCGCATTTGCAGAAATGGGGCCCATCTGGAGAGACACAC 2022
Qy 1975 AAACTAGAAGTATCATCTGAGAGAGTCTATGAGTTCAGACTACGCTGAGCAAACTGATC 2034
Db 2023 AAGTTGGAAGTATCATCTGAGAAATCTATGATTCAGAGTACTGTGAGCAAACTCAT 2082
Qy 2035 AAGAAGACAAACCTGGCCCTTGGTGGGGACCAATTCCTGAGAGACAGTTCAATGAG 2094
Db 2083 AAGAAGACAAACCTGGCCCTTGGTGGAGTAAACAGCTGAGAGAACAGTTCAATGAA 2142
Qy 2095 GCCATACCCGTCAGTCAGACAGAGGAGATGAGATGAATCCGGGAGAGAGAGCTG 2154
Db 2143 GCTATCAGTGTGAGTGGGGAAGATGATGAGAGATGATGAGAGAGAGAGAGCTG 2202
Qy 2155 CCTCTCTGCTTGTACTAGTCAATGCACCTTCGACTGTCTTGTGAAAGTGTCTTTGCC 2214
Db 2203 CCTCTCTGCTTGTACTAGTCAATGCACCTTCGACTGTCTTGTGAAAGTGTCTTTGCC 2262
Qy 2215 TGTGTGCCCCCAGAGTACGACAGGCTGGGCTGCTTGGCGCTTCACATCCCTCATC 2274
Db 2263 TTTGTCCTCCCTACGAAATGAGAAATGGCTGGGCTGTTTCAATGCTTCATCCCTCATG 2322
Qy 2275 ATTGCATGCTACCGCCATCATTTGGGAGCTGGCCCTGCACCTTCGAGCAATGGT 2334
Db 2323 ATTTGGCTCTACAGACTTTCATTTGGAGACTGGCTTCCCACTTGGCTGCACATTTGGC 2382
Qy 2335 CTCAAGATTTCAGTACAGACTGTTTTCGTGGCAATTTGGCACTGTGCCAGATAG 2394
Db 2383 CTGAAGATTTCGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2442
Qy 2395 TTTGGCAGCAAGAGTGTGCTCCAGAGTGTATATGACAGAGCTTCATTTGGCAAGCTG 2454
Db 2443 TTTGGCAGCAAGAGTGTGCTCCAGAGTGTATATGACAGAGCTTCATTTGGCAAGCTG 2502
Qy 2455 ACGGAGCAGCAAGCCTCATATGTTCTGCTGGGCACTGGGCTGCTGCTGCTGCTGCTG 2514
Db 2503 ACGGAGCAGCAAGCCTGATATGTTCTTCTGGAATGCTGCTGCTGCTGCTGCTGCTG 2562
Qy 2515 ATCTACTGGGCTCTGAGGAGACAGAGTTCACGTGTGGCCGACACTGGCTGCTTCTC 2574
Db 2563 ATCTACTGAGCAGCAAGTATGAGTTCACAAAGTGTCCCTGGCAGCTTACTTCTCT 2622
Qy 2575 GTACACCTCTTACACATCTTGTGATGCTGATCAGGCTGCTGCTGCTGCTGCTGCTG 2634
Db 2623 GTACACCTCTTACACATCTTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 2682
Qy 2635 CCGCACCTGGAGGAGCTTGTGGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694

Db 2683 CCAGAAATCGAGGTGAGCTGGGTGGGCCCCGAGCTGCCAAGCTCCTCATCTGCTC 2742
Qy 2695 TTTGAGAGCTGTGGCTCTCTACATCTTTGGCAGACTAGAGGCTTATGCTACATC 2754
Db 2743 TTTGCTCTCTATGGCTTGTGACATTTTCTCTCTCTGAGGCTTACTGCCACATA 2802
Qy 2755 AAGGCTTCTAA 2766
Db 2803 AAGGCTTCTAA 2814

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